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Conference Abstract

Global Genome Biodiversity Network - Infrastructure for genomic research

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Abstract

Genomic research depends upon access to DNA or tissue collected and preserved according to high-quality standards. At present, the collections in most natural history museums do not sufficiently address these standards. In response to these challenges, natural history museums, culture collections, herbaria, botanical gardens and others have started to build high-quality biodiversity biobanks. Unfortunately, information about these collections remains fragmented, scattered and largely inaccessible. Without a central registry of relevant institutions, it is difficult and time-consuming to locate the needed samples.

The Global Genome Biodiversity Network (GGBN) was created to fill this gap by establishing a central access point for locating samples meeting quality standards for genome-scale applications, while complying with national and international legislations and conventions (e.g. the Nagoya Protocol). The GGBN is rapidly growing and currently has 70 members and works closely together with GBIF, SPNHC, CETAF, INSDC, BOLD, ESBB, ISBER, GSC and others to reach its goals.

Knowledge of biodiversity biobank content is urgently needed to enable concerted efforts and strategies in collecting and sampling new material and making ABS a reality. GGBN provides an infrastructure for making genomic samples discoverable and accessible.

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While respecting national law, GGBN requires that its members comply with the provisions of the Nagoya-protocol. Thus researchers, collection-holding institutions, and networks should adopt a common Best Practice approach to manage ABS, as has been developed by GGBN. A Code of Conduct; recommendations for implementing the Code of Conduct (the Best Practices), and implementation tools, such as standard Material Transfer Agreements (MTA) and mandatory and recommended data fields in collection databases, are tools which will aid compliance. This talk provides an overview of GGBN and comprises updates on GGBN's best practices on ABS and the Nagoya Protocol, with examples of their use and applicability.

Keywords

Global Genome Biodiversity Network, biodiversity biobanks, molecular collections, best practices, access and benefit sharing, genomic research infrastructure

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